

In the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims

1-7. (Canceled)

8. (Currently amended) The A method according to claim 13 or claim 14~~claim 4~~, wherein the restriction ~~site enzyme recognition sequence~~ is specific for a class IIs enzyme.

9. (Currently amended) The A method according to claim 8, wherein the enzyme is SfaNI or Earl.

10. (Currently amended) The A method according to claim 13 or claim 14~~claim 5~~, wherein the polymerase reaction is carried out using methyl-dCTP as a replacement for dCTP.

11. (Currently amended) The A method according to claim 13 or claim 14~~claim 2~~, wherein the adapter is immobilised on a support material.

12. (Currently amended) The A method according to claim 13 or 14~~claim 6~~, wherein sequential signal sequences and optionally sequential adapters comprise recognition sites for different oligonucleotide primers.

13. (Currently amended) A method for determining the sequence of a target polynucleotide, comprising the steps of:

i) treating a sample of a double-stranded target polynucleotide to create overhangs at each end, one of which is to be sequenced, each overhang having a defined number of bases;

ii) dividing the sample into reaction compartments and contacting each separate sample with a double-stranded polynucleotide signal sequence and a corresponding double stranded adapter polynucleotide, each signal sequence representing a specific polynucleotide sequence of the same length as that of the overhang to be sequenced and comprising an

overhang that permits hybridisation and ligation to the end of the target polynucleotide opposite that being sequenced, and each adapter comprising an overhang that is of complementary sequence to the sequence represented by the signal sequence, wherein the adapter will hybridise to the overhang on the target sample that is to be sequenced only if the sequence of the adapter overhang sequence is complementary to the overhang that is being sequenced;

iii) carrying out the polymerase reaction on the sample (s) using primers that hybridise at the ends of the signal sequence and adapter sequence, wherein the product of the polymerase reaction comprises a restriction site that permits cleavage of the adapter to form a new overhang to be sequenced optionally by repeating steps (i) to (iii) using restriction enzymes to create the overhangs;

and iv) identifying which signal sequences are present on the amplified products, and in which order, to thereby determine the sequence of the target polynucleotide.

14. (Currently amended) The A method according to claim 13, wherein the overhang that ligates to the signal sequence is at least 3 bases.

15. (Currently amended) The A method according to claim 13 or claim 14, wherein the overhang to be sequenced is 4 bases.

16. (New) The method according to claim 13 or claim 14, wherein the combination of all the sequences represented by the signal sequence in each reaction compartment corresponds to all the permutations of a sequence comprising the number of bases in the overhang to be sequenced.